

1648

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/147,801C

DATE: 05/03/2001
TIME: 12:55:28

Input Set : A:\3786002.app
Output Set: N:\CRF3\05032001\I147801C.raw

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3 <110> APPLICANT: NIKLASSON, BO
5 <120> TITLE OF INVENTION: NEW PICORNAVIRUSES, VACCINES AND DIAGNOSTIC KITS
7 <130> FILE REFERENCE: 03786.002
9 <140> CURRENT APPLICATION NUMBER: 09/147,801C
10 <141> CURRENT FILING DATE: 1999-03-11
12 <150> PRIOR APPLICATION NUMBER: PCT/SE97/01515
13 <151> PRIOR FILING DATE: 1997-09-09
15 <160> NUMBER OF SEQ ID NOS: 20
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 264
21 <212> TYPE: DNA
22 <213> ORGANISM: Ljungan virus
24 <400> SEQUENCE: 1
25 agtctagtct tatcttgtat gtgtcctgca ctgaacttgt ttctgtctct ggagtgtctct 60
26 acacttcagt aggggctgta cccgggcggt cccactcttc acaggaatct gcacaggtgg 120
27 ctttcacctc tggacagtgc attccacacc cgctccacgg tagaagatga tgtgtgtctt 180
28 tgcttgtgaa aagcttgtga aaatcgtgtg taggcgtagc ggctacttga gtgccagcgg 240
29 attacccta gtgtaacac tagc 264
32 <210> SEQ ID NO: 2
33 <211> LENGTH: 264
34 <212> TYPE: DNA
35 <213> ORGANISM: Ljungan virus
37 <220> FEATURE:
38 <221> NAME/KEY: modified_base
39 <222> LOCATION: (1)..(264)
40 <223> OTHER INFORMATION: "n" represents a, t, c, g, other or unknown
42 <400> SEQUENCE: 2
43 agtctagttt cattctgtgt gtgtttggca ctgaaattat ttctgtctct ggggtgcttt 60
W--> 44 acacttcagt aggggctgta cccgggcggt cccactcttc acaggaatnt gcacaggtgg 120
45 ctttcacctc tggacagtgc attccacacc cgctccacag tagaagatga tgtgtgtctt 180
W--> 46 tgcttgtgaa aagcttgtga aaatcgtgtg taggcgtagc ggntacttga gtgccagcgg 240
W--> 47 acnacccta gtgtaacac tagc 264
50 <210> SEQ ID NO: 3
51 <211> LENGTH: 264
52 <212> TYPE: DNA
53 <213> ORGANISM: Ljungan virus
55 <400> SEQUENCE: 3
56 agtttggttc tctcttgagt gtgttttgtg ttagcataat ttctgtctct agagtgtctt 60
57 acactctagt aggggctgta cccgggcggt cccactcttc acaggaatct gcacaggtgg 120
58 ctttcacctc tggacagtgc attccatacc cgctccacaa tagaagatga tgtatatctt 180
59 tgtttgtgaa atgctcatga aacgtgtgtg taggcgtagc ggctacttga atgccagcgg 240
60 aaccccta gtgtaacac tagc 264
63 <210> SEQ ID NO: 4
64 <211> LENGTH: 179
65 <212> TYPE: PRT
66 <213> ORGANISM: Ljungan virus

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68 <400> SEQUENCE: 4

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69 Lys Asp Leu Met Glu Ile Ala Arg Met Pro Ser Val Tyr Lys Gly Glu
70   1           5           10           15
72 Arg Thr Glu Pro Gly Gly Thr Asn Gly Tyr Phe Gln Trp Ser His Thr
73           20           25           30
75 His Ser Pro Ile Asn Trp Val Phe Asp Gly Gly Ile His Leu Glu Asp
76           35           40           45
78 Met Pro Asn Leu Asn Leu Phe Ser Ser Cys Tyr Asn Tyr Trp Arg Gly
79           50           55           60
81 Ser Thr Val Leu Lys Leu Thr Val Tyr Ala Ser Thr Phe Asn Lys Gly
82   65           70           75           80
84 Arg Leu Arg Met Ala Phe Phe Pro Ile Met Met Gln Gly Thr Gln Arg
85           85           90           95
87 Lys Lys His Lys Cys Leu Phe Met Val Cys Asp Ile Gly Leu Asn Asn
88           100          105          110
90 Thr Phe Glu Met Thr Ile Pro Tyr Thr Trp Gly Asn Trp Met Arg Pro
91           115          120          125
93 Thr Arg Gly Ser Val Ile Gly Trp Leu Arg Ile Asp Val Leu Asn Arg
94           130          135          140
96 Leu Thr Tyr Asn Ser Ser Ser Pro Asn Ala Val Asn Cys Ile Leu Gln
97 145           150          155          160
99 Val Lys Met Gly Asn Asp Ala Lys Phe Met Val Pro Thr Thr Ser Asn
100           165          170          175

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102 Ile Val Trp

106 <210> SEQ ID NO: 5

107 <211> LENGTH: 241

108 <212> TYPE: DNA

109 <213> ORGANISM: Cardiovirus

111 <400> SEQUENCE: 5

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112 tgacagggtt attttcacct cttcttttct actccacagt gttctatact gtggaagggt 60
113 atgtgttgcc ccttccttct tggagaacgt gcgcggcggt ctttccgtct ctcgacaagc 120
114 gcgcgtgcaa catacagagt aacgcgaaga aagcagttct cgtctagct ctagtgccca 180
115 caagaaaaca gctgtagcga ccacacaaag gcagcggaac cccctcctg gtaacaggag 240
116 c                                     241

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119 <210> SEQ ID NO: 6

120 <211> LENGTH: 243

121 <212> TYPE: DNA

122 <213> ORGANISM: Cardiovirus

124 <400> SEQUENCE: 6

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125 tgacagggtt attttcacct cttctctctt ctacttcata gtgttctata ctatgaaagg 60
126 gtatgtgtcg ccccttcctt cttggagaac gtgcgtggcg gtctttccgt ctctcgaaaa 120
127 acgtgcgtgc gacatgcaga gtaacgcaaa gaaagcagtt cttggtctag ctctgggtgc 180
128 cacaagaaaa cagctgtagc gaccacacaa aggcagcgga aaccctctcc tggtaacagg 240
129 agc                                     243

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132 <210> SEQ ID NO: 7

133 <211> LENGTH: 247

134 <212> TYPE: DNA

135 <213> ORGANISM: Cardiovirus

137 <400> SEQUENCE: 7

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138 aggccggtgt gcgtttgtct atatgttatt ttccaccata ttgccgtcctt ttggcaatgt 60
 139 gagggcccg aaacctggcc ctgtcttctt gacgagcatt cctaggggtc ttccccctct 120
 140 cgccaaagga atgcaaggtc tggtgaatgt cgtgaaggaa gcagttcctc tggaagcttc 180
 141 ttgaagacaa acaacgtctg tagcgacct ttgcaggcag cggaaccccc cacctggcga 240
 142 caggtgc 247

145 <210> SEQ ID NO: 8

146 <211> LENGTH: 188

147 <212> TYPE: PRT

148 <213> ORGANISM: Cardiovirus

150 <400> SEQUENCE: 8

151 Ser Asp Leu Leu Glu Leu Cys Lys Leu Pro Thr Phe Leu Gly Asn Pro

152 1 5 10 15

154 Asn Thr Asn Asn Lys Arg Tyr Pro Tyr Phe Ser Ala Thr Asn Ser Val

155 20 25 30

157 Pro Ala Thr Ser Met Val Asp Tyr Gln Val Ala Leu Ser Cys Ser Cys

158 35 40 45

160 Met Ala Asn Ser Met Leu Ala Ala Val Ala Arg Asn Phe Asn Gln Tyr

161 50 55 60

163 Arg Gly Ser Leu Asn Phe Leu Phe Val Phe Thr Gly Ala Ala Met Val

164 65 70 75 80

166 Lys Gly Lys Phe Leu Ile Ala Tyr Thr Pro Pro Gly Ala Gly Lys Pro

167 85 90 95

169 Thr Thr Arg Asp Gln Ala Met Gln Ser Thr Tyr Ala Ile Trp Asp Leu

170 100 105 110

172 Gly Leu Asn Ser Ser Phe Asn Phe Thr Ala Pro Phe Ile Ser Pro Thr

173 115 120 125

175 His Tyr Arg Gln Thr Ser Tyr Thr Ser Pro Thr Ile Thr Ser Val Asp

176 130 135 140

178 Gly Trp Val Thr Val Trp Lys Leu Thr Pro Leu Thr Tyr Pro Ser Gly

179 145 150 155 160

181 Thr Pro Thr Asn Ser Asp Ile Leu Thr Leu Val Ser Ala Gly Asp Asp

182 165 170 175

184 Phe Thr Leu Arg Met Pro Ile Ser Pro Thr Lys Trp

185 180 185

188 <210> SEQ ID NO: 9

189 <211> LENGTH: 188

190 <212> TYPE: PRT

191 <213> ORGANISM: Cardiovirus

193 <400> SEQUENCE: 9

194 Ser Asp Leu Leu Glu Leu Cys Lys Leu Pro Thr Phe Leu Gly Asn Pro

195 1 5 10 15

197 Ser Thr Asp Asn Lys Arg Tyr Pro Tyr Phe Ser Ala Thr Asn Ser Val

198 20 25 30

200 Pro Ala Thr Ser Leu Val Asp Tyr Gln Val Ala Leu Ser Cys Ser Cys

201 35 40 45

203 Met Ala Asn Ser Met Leu Ala Ala Val Ala Arg Asn Phe Asn Gln Tyr

204 50 55 60

206 Arg Gly Ser Leu Asn Phe Leu Phe Val Phe Thr Gly Ala Ala Met Val

207 65 70 75 80

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209 Lys Gly Lys Phe Arg Ile Ala Tyr Thr Pro Pro Gly Ala Gly Lys Pro
210      85      90      95
212 Thr Thr Arg Asp Gln Ala Met Gln Ala Thr Tyr Ala Ile Trp Asp Leu
213      100      105      110
215 Gly Leu Asn Ser Ser Phe Asn Phe Thr Ala Pro Phe Ile Ser Pro Thr
216      115      120      125
218 His Tyr Arg Gln Thr Ser Tyr Thr Ser Pro Thr Ile Thr Ser Val Asp
219      130      135      140
221 Gly Trp Val Thr Val Trp Gln Leu Thr Pro Leu Thr Tyr Pro Ser Gly
222 145      150      155      160
224 Thr Pro Thr Asn Ser Asp Ile Leu Thr Leu Val Ser Ala Gly Asp Asp
225      165      170      175
227 Phe Thr Leu Arg Met Pro Ile Ser Pro Thr Lys Trp
228      180      185
231 <210> SEQ ID NO: 10
232 <211> LENGTH: 188
233 <212> TYPE: PRT
234 <213> ORGANISM: Cardiovirus
236 <400> SEQUENCE: 10
237 Ser Asp Leu Leu Glu Leu Cys Lys Leu Pro Thr Phe Leu Gly Asn Pro
238 1      5      10      15
240 Ser Thr Asp Asn Lys Arg Tyr Pro Tyr Phe Ser Ala Thr Asn Ser Val
241      20      25      30
243 Pro Ala Thr Ser Leu Val Asp Tyr Gln Val Ala Leu Ser Cys Ser Cys
244      35      40      45
246 Met Ala Asn Ser Met Leu Ala Ala Val Ala Arg Asn Phe Asn Gln Tyr
247      50      55      60
249 Arg Gly Ser Leu Asn Phe Leu Phe Val Phe Thr Gly Ala Ala Met Val
250 65      70      75      80
252 Lys Gly Lys Phe Leu Ile Ala Tyr Thr Pro Pro Gly Ala Gly Lys Pro
253      85      90      95
255 Thr Thr Arg Asp Gln Ala Met Gln Ala Thr Tyr Ala Ile Trp Asp Leu
256      100      105      110
258 Gly Leu Asn Ser Ser Phe Asn Phe Thr Ala Pro Phe Ile Ser Pro Thr
259      115      120      125
261 His Tyr Arg Gln Thr Ser Tyr Thr Ser Pro Thr Ile Thr Ser Val Asp
262      130      135      140
264 Gly Trp Val Thr Val Trp Gln Leu Thr Pro Leu Thr Tyr Pro Ser Gly
265 145      150      155      160
267 Thr Pro Thr Asn Ser Asp Ile Leu Thr Leu Val Ser Ala Gly Asp Asp
268      165      170      175
270 Phe Thr Leu Arg Met Pro Ile Ser Pro Thr Lys Trp
271      180      185
274 <210> SEQ ID NO: 11
275 <211> LENGTH: 188
276 <212> TYPE: PRT
277 <213> ORGANISM: Cardiovirus
279 <400> SEQUENCE: 11
280 Ser Asp Leu Leu Glu Leu Cys Lys Leu Pro Thr Phe Leu Gly Asn Pro

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281      1              5              10              15
283 Asn Ser Asn Asn Lys Arg Tyr Pro Tyr Phe Ser Ala Thr Asn Ser Val
284              20              25              30
286 Pro Thr Thr Ser Leu Val Asp Tyr Gln Val Ala Leu Ser Cys Ser Cys
287              35              40              45
289 Met Ala Asn Ser Met Leu Ala Ala Val Ala Arg Asn Phe Asn Gln Tyr
290              50              55              60
292 Arg Gly Ser Leu Asn Phe Leu Phe Val Phe Thr Gly Ala Ala Met Val
293 65              70              75              80
295 Lys Gly Lys Phe Leu Ile Ala Tyr Thr Pro Pro Gly Ala Gly Lys Pro
296              85              90              95
298 Thr Thr Arg Asp Gln Ala Met Gln Ala Thr Tyr Ala Ile Trp Asp Leu
299              100              105              110
301 Gly Leu Asn Ser Ser Phe Val Phe Thr Ala Pro Phe Ile Ser Pro Thr
302              115              120              125
304 His Tyr Arg Gln Thr Ser Tyr Thr Ser Ala Thr Ile Ala Ser Val Asp
305 130              135              140
307 Gly Trp Val Thr Val Trp Gln Leu Thr Pro Leu Thr Tyr Pro Ser Gly
308 145              150              155              160
310 Ala Pro Val Asn Ser Asp Ile Leu Thr Leu Val Ser Ala Gly Asp Asp
311              165              170              175
313 Phe Thr Leu Arg Met Pro Ile Ser Pro Thr Lys Trp
314              180              185
317 <210> SEQ ID NO: 12
318 <211> LENGTH: 187
319 <212> TYPE: PRT
320 <213> ORGANISM: Cardiovirus
322 <220> FEATURE:
323 <221> NAME/KEY: MOD_RES
324 <222> LOCATION: (102)
325 <223> OTHER INFORMATION: variable or unknown amino acid
327 <400> SEQUENCE: 12
328 Thr Asp Leu Leu Glu Leu Cys Lys Leu Pro Thr Phe Leu Gly Asn Leu
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331 Ser Asn Asp Thr Arg Val Pro Phe Phe Thr Ala Thr Asn Ser Val Pro
332              20              25              30
334 Thr Glu Ser Leu Val Glu Tyr Gln Val Thr Leu Ser Cys Ser Cys Met
335              35              40              45
337 Ser Asn Ser Met Leu Ala Ser Val Ala Arg Asn Phe Asn Gln Tyr Arg
338 50              55              60
340 Gly Ser Leu Asn Phe Leu Phe Val Phe Thr Gly Ser Ala Met Thr Lys
341 65              70              75              80
343 Gly Lys Phe Leu Ile Ala Tyr Thr Pro Pro Gly Ala Gly Lys Pro Thr
344              85              90              95
346 Thr Arg Asp Gln Ala Xaa Gln Ser Thr Tyr Ala Ile Trp Asp Leu Gly
347              100              105              110
349 Leu Asn Ser Ser Phe Asn Phe Thr Val Pro Phe Ile Ser Pro Ser His
350 115              120              125
352 Tyr Arg Gln Thr Ser Tyr Thr Ser Pro Ser Ile Ala Ala Val Asp Gly

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VERIFICATION SUMMARY

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Input Set : A:\3786002.app

Output Set: N:\CRF3\05032001\I147801C.raw

L:44 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:47 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12